

WHAT IS CLAIMED IS:

1. A DNA construct comprising as operably linked components in the direction of transcription, a promoter region obtainable from a gene selected from the group consisting of a napin gene, an EA9 gene or an acyl carrier protein gene; a DNA sequence of interest other than the native coding sequence of said gene; and a transcription termination region, wherein said components are functional in a plant cell, and wherein said DNA construct is flanked by T-DNA.

2. The DNA construct according to Claim 1, wherein said DNA sequence of interest encodes an enzyme.

3. The DNA construct according to Claim 1, wherein said DNA sequence of interest is an antisense sequence.

4. A plant cell having an altered phenotype as a result of expression of a DNA construct according to Claim 1.

5. The plant cell according to Claim 4, wherein said DNA construct is flanked by T-DNA.

6. The plant cell according to Claim 5 wherein said cell is one from the group consisting of a soybean cell and a rapeseed cell.

7. The plant cell according to Claim 4, wherein said DNA sequence of interest encodes an enzyme.

8. The plant cell according to Claim 4, wherein said DNA sequence of interest is an antisense sequence.

9. A plant comprising cells comprising a DNA construct according to any one of Claims 1-3.

10. The plant according to Claim 9, wherein said plant is dicotyledonous.

11. Seed obtained from a plant according to Claim 10.

12. Seed having a DNA construct according to Claim 1.

13. The seed according to Claim 12, wherein said seed is an oil seed or a grain seed.

14. The seed according to Claim 12, wherein said seed is from a dicotyledonous plant.

15. The seed according to Claim 14, wherein said seed is from a plant of the genus *Brassica*.

16. The seed according to Claim 14, wherein said dicotyledonous plant is selected from the group consisting of cotton, soybean, safflower and sunflower.

17. A method for obtaining a plant having a modified phenotype, said method comprising;

transforming a host plant cell with a DNA construct under genomic integration conditions, wherein said construct comprises as operably linked components in the direction of transcription, a promoter region obtainable from a gene, wherein transcription of said gene is regulated in plant seed tissue, a DNA sequence of interest other than the native coding sequence of said gene, and a transcription termination region, wherein said components are functional in a plant cell,

whereby said DNA construct becomes integrated into a genome of said plant cell;

regenerating a plant from said transformed plant cell, and growing said plant under conditions whereby said DNA sequence of interest is expressed and a plant having said modified phenotype is obtained.

18. A method for altering the phenotype of plant seed tissue as distinct from other plant tissue, said method comprising:

growing a plant, wherein said plant comprises cells containing a DNA construct integrated into their genome, said DNA construct comprising, in the 5' to 3' direction of transcription, a transcriptional initiation region from a gene, wherein transcription of said gene is regulated in a plant seed tissue, a DNA sequence of interest other than the coding sequence native to said transcriptional initiation region, and a transcriptional termination region, whereby said DNA sequence of interest is transcribed under transcriptional control of said transcriptional initiation region and a plant having an altered phenotype is obtained.

19. The method according to Claim <sup>1</sup>17 or <sup>2</sup>18, wherein said DNA construct is flanked by T-DNA.

20. The method according to Claim 19, wherein said plant is a soybean or rapeseed plant.

<sup>5</sup>  
~~21.~~ The method according to Claim ~~17~~<sup>1</sup> or ~~18~~<sup>2</sup> wherein said DNA sequence of interest encodes an enzyme.

<sup>6</sup>~~22.~~ The method according to Claim ~~17~~<sup>1</sup> or ~~18~~<sup>2</sup> wherein said DNA sequence of interest is an antisense sequence.

~~Sub C4~~ ~~23.~~ The method according to Claim ~~17~~ or ~~18~~ wherein said gene is transcribed during seed embryogenesis.

~~24.~~ The method according to Claim 23 wherein said gene is transcribed from about day 7 to day 40 postanthesis.

<sup>7</sup>~~25.~~ The method according to Claim ~~17~~<sup>1</sup> or ~~18~~<sup>2</sup> wherein said gene is transcribed during seed maturation.

~~Sub C5~~ ~~26.~~ The method according to Claim 25 wherein said gene is transcribed from about day 11 to day 30 postanthesis.

<sup>13</sup>~~27.~~ The method according to Claim ~~18~~<sup>2</sup> wherein said transcriptional initiation region further comprises a translational initiation region and said DNA sequence of interest is an open reading frame encoding an amino acid sequence.

~~Sub E3~~ ~~28.~~ A method for modifying the genotype of a plant to impart a desired characteristic to seed as distinct from other plant tissue, said method comprising:

transforming under genomic integration conditions, a host plant cell with a DNA construct comprising in the 5' to 3' direction of transcription, a transcriptional initiation region from a gene, wherein transcription of said gene is regulated in a plant seed tissue, a DNA sequence of interest other than the native coding sequence of said gene, and a transcriptional termination region, whereby said DNA construct becomes integrated into the genome of said plant cell;

regenerating a plant from said transformed host cell; and growing said plant to produce seed having a modified genotype.

<sup>19</sup>~~29.~~ The method according to Claim ~~28~~<sup>18</sup>, wherein said DNA construct is flanked by T-DNA.

<sup>20</sup>~~30.~~ The method according to Claim ~~28~~<sup>18</sup>, wherein said plant is a Brassica plant.

<sup>21</sup>~~31.~~ The method according to Claim ~~28~~<sup>18</sup>, wherein said DNA sequence of interest encodes an enzyme.

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~~32.~~ The method according to Claim ~~28~~, wherein said DNA sequence of interest is an antisense sequence.

~~Sub 07-33.~~ The method according to Claim 28, wherein said plant is a soybean plant.

34. A method for modifying transcription in seed tissue as distinct from other plant tissue, said method comprising:

growing a plant capable of developing seed tissue under conditions to produce seed, wherein said plant comprises cells containing a DNA construct integrated into their genome, said DNA construct comprising, in the 5' to 3' direction of transcription, a seed-specific transcriptional initiation region, a DNA sequence of interest other than the coding sequence native to said transcriptional initiation region, and a transcriptional termination region, whereby said DNA sequence of interest is transcribed under transcriptional control of said seed-specific transcription initiation region.

~~25~~ 35. The method according to Claim ~~34~~, wherein said DNA sequence of interest is an antisense sequence.

~~26~~ 36. The method according to Claim ~~34~~, wherein said plant is of the genus *Brassica*.

~~27~~ 37. The method according to Claim ~~34~~, wherein said transcriptional initiation region further comprises a translational initiation region and said DNA sequence of interest is an open reading frame encoding an amino acid sequence.

~~Sub 08~~ 38. The method according to Claim 34, wherein said plant is a soybean plant.

39. A method to selectively express a heterologous DNA sequence of interest in seed tissue as distinct from other plant tissue, said method comprising:

growing a plant capable of developing seed tissue under conditions to produce seed, wherein said plant comprises cells having a genomically integrated DNA construct comprising, as operably linked components in the 5' to 3' direction of transcription, a seed-specific transcriptional initiation region and a translational initiation region, a DNA sequence of interest other than the coding sequence native to said transcriptional

*Sub E5* [initiation region, a transcriptional termination region downstream of said DNA sequence of interest, whereby said DNA sequence of interest is expressed under control of said seed-specific transcriptional and translational initiation region.

*30* 40. The method according to Claim *39*,<sup>29</sup> wherein said plant is of the genus *Brassica*.

*Sub C9* 41. The method according to Claim 39, wherein said plant is a soybean plant.

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*4*  
*C11*

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